# International Trade Implications of Highly Pathogenic Poultry Disease Events

# Jada M. Thompson , Dustin L. Pendell, Amy D. Hagerman, and Kamina K. Johnson

Animal disease events can lead to international trade restrictions which can vary in duration, products included, and geographical extent. Accounting for multilateral resistance between trading partners, a general gravity model of trade is estimated with a Hausman-Taylor and a Hausman-Taylor seemingly unrelated estimator to evaluate the trade quantity impact by commodity resulting from highly pathogenic poultry disease events in 24 exporting markets. Commodity specific results show that quantity traded and products demanded during a disease event differ by commodities. Understanding these impacts can better prepare exporters for potential changes in trade quantity given a disease event.

Key words: International Trade, Poultry, Animal Diseases, Econometric Modeling

#### Introduction

Global consumer demand for meat has steadily increased over the last half century and is projected to continue to increase. Total global per capita consumption for all meat, including beef, pork, poultry, lamb, and mutton, was 73.6 pounds per capita in 2010, 75.2 pounds per capita in 2015, and is projected to be 76.7 pounds per capita in 2020 according to the Organisation for Economic Co-operation and Development (OECD) (2016). Poultry products have been gaining in popularity as an affordable source of protein, globally surpassing pork consumption in 2007 to be the most-consumed per capita protein source. Export markets and factors that affect those markets are important to animal industries, especially if there are processes to mitigate disruptions in trade or ways to best respond to accommodate changes in trade.

International trade disruptions can cause negative and costly impacts to both exporting and importing countries. Disease events in animal agriculture can cause severe disruptions in trade and result in costs along the supply chain,

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including the cost of mitigation or eradication of a disease (Paarlberg et al. 2009; Pendell et al. 2015). Management of highly pathogenic disease events can contribute to potential trade disruptions or aid in reducing potential impacts (Marsh, Wahl, and Suyambulingam 2005; Seitzinger and Paarlberg 2016). It is important for animal disease managers to understand the potential market disruptions and the associated costs that result from an animal health event as they prepare for future outbreaks.

Highly pathogenic avian influenza (HPAI) and Newcastle disease virus (NDV) are of particular concern to the poultry industry due to their high mortality rates and potential economic losses. Some strains have the potential for zoonosis (being a disease transmissible from animals to humans, from either direct contact or carried by a vector). An outbreak of HPAI in the United States (2014–2015) resulted in depopulation of 49.6 million birds and cost more than \$950 million dollars to U.S. taxpayers (Seitzinger and Paarlberg 2016; USDA-APHIS, 2016). Trade restrictions from importing countries and reduction in bird stocks resulted in declined U.S. poultry exports in 2015, the first time since 2006 (Seitzinger and Paarlberg 2016; USDA-FAS, 2016). There were two additional outbreaks of HPAI in 2016 and 2017 in Indiana and Tennessee, respectively, that were limited in geographic scope and had minimal affected bird populations and negligible trade implications.

Globally, according to the World Organisation for Animal Health (OIE), between 2000 and 2015 there were more than 400 distinct HPAI or NDV disease events in non-endemic regions, or those regions in which a disease is not regularly found (OIE 2015). Each of these events had implications for domestic markets and potentially affected the global market. While there were limited HPAI events in 2016 and 2017, these had negligible international responses considering there was an international movement toward proactive regionalized strategies not available in earlier periods of this study. The objective of this article is to analyze the impact of trade disruptions as a result of disease events affecting poultry trade at a granular level not found in current literature. Disaggregated, individual product categories are modeled to determine the bilateral trade flows impacts during a disease event and whether these differ by poultry product category, using a series of estimators.

# **Background**

Animal disease events are one of many sudden occurrences that may lead to trade disruptions in animal agriculture. An importing country's response to a highly pathogenic disease event is a complex process but can be decomposed into two broad questions. First, does the animal disease situation warrant a limitation on trade of meat or animal products from the affected exporting country? Second, if a limitation is warranted, what should the scope of that limitation be? The scope of the limitations can be measured in terms of the relative risk posed by various product categories, the geographic extent of the event, and/or the duration of limitations. Each of these decisions

intensifies or lessens the burden of trade restrictions imposed on exporting countries.

Trade restriction decisions are complex in terms of affected commodities, and there is no central repository to record the specific embargoes for historical disease events. The composition of products traded can change markedly during a disease event as substitutions can occur between fresh, frozen, and prepared products depending on the importer preference and risk acceptance. Products viewed as having minimal risk for disease spread may be preferential to a risk averse importing country than other products with greater potential for disease spread. The previous studies discussed, as well as other commodity trade analyses, typically aggregate commodities to a high level, which can over or underestimate the effects on individual product categories. Poultry product categories separate commodities into species, processing level, and cut. Importer responses to animal health events can vary by species (e.g., chicken or turkey), cut (e.g., whole or parts), and/or degree of processing (e.g., fresh or frozen) for meat and egg products based on trade policies and consumer demand impacts (Mu et al. 2015; Hasiner and Yu 2018). For example, whole fresh chicken may have a different trade response than cooked chicken products which have been shown to be safe to consume if properly handled (Chmielewski and Swayne 2011). For the poultry industry, the categories of products being exported and the nature of a disease event, such as whether the disease is limited to wild birds or a strain that is potentially zoonotic, are important influencing factors of trade. The dynamic effects of the disease and how long the effects of HPAI and NDV have on trade, such as with Mu et al. (2015), are not estimated with this data. The focus of this work is to estimate the magnitudinal effects of HPAI and NDV in aggregate and across commodities. Future research could expand this analysis to the dynamic implications of trade restrictions due to a disease event.

Previous analyses of highly pathogenic avian diseases estimated the time it takes for export market revenue to recover after a disease event (Johnson et al. 2015) and the impact on United States domestic markets (Brown et al. 2007; Djunaidi and Djunaidi 2007; Johnson et al. 2014; Miller and Parent 2012). Disease control measures and uncertainty in trade embargoes have been shown to exacerbate the effects of a disease disruption (Rich and Winter-Nelson 2007; Ruhl 2011; Wang and Hennessy 2015). Johnson et al. (2015) used a zero-inflated negative binomial model to determine recovery time for exporting countries' trade value. The authors determined that several factors, including type of domestic production and origin of exports, led to extended export revenue recovery times. Thompson (2018) determined that the geographical scope of trade restrictions impacts the quantity demanded during the 2014-2015 HPAI outbreak, and these changes impact disaggregated commodities differently.

This article extends previous literature by analyzing the bilateral trade implications on quantity of poultry products traded during a highly pathogenic disease event for specific product categories as defined by the Harmonized Commodity Description and Coding Systems (HS) (see Table 1). Monthly bilateral trade and disaggregated commodity groups were used to measure the consequences of highly pathogenic disease events on specific products, both in cut and degree of processing. Results provide timely, policy relevant information of bilateral trade disruptions during an animal health event.

# Methodology

The gravity model of trade has been widely used in the trade literature to analyze bilateral trade (Bergstrand 1985; Isard 1954; Tinbergen 1962). The basic gravity specification, shown in Equation 1, expresses the quantity traded  $(Y_{i,j,t})$  between countries i and j in time t as a function of a proportional constant term (C), the mass (M) of both i and j countries (typically expressed using country gross domestic product [GDP] or population weighted GDP), and the distance  $(d_{i,j})$  from i to j. Finally,  $\beta_1$  is the trade flow creation parameter,  $\beta_2$  is the trade flow attraction parameter, and  $\beta_3$  is the trade flow resistance parameter.

(1) 
$$Y_{i,j,t} = C \frac{M_i^{\beta_1} M_j^{\beta_2}}{d_{i,j}^{\beta_3}}$$

To estimate the gravity model, the natural logarithm of the theoretical model is taken. The logged form of the basic gravity model is given in Equation 2, where K is a logged constant term for C and  $\varepsilon_{i,i,t}$  represents an error term:

(2) 
$$ln Y_{i,j,t} = K + \beta_1 ln M_i + \beta_2 ln M_j + \beta_3 ln d_{i,j} + \varepsilon_{i,j,t}$$

The basic model was later expanded to include additional multiplicative factors that influence trade, including trade agreements (Grant and Lambert 2008; Martínez-Zarzoso and Nowak-Lehmann 2003).

Despite being an effective model of trade, the gravity model requires an increasing number of indicator variables to account for nuances in bilateral trading relationships (Salvatici 2013; Serlenga and Shin 2007). Many factors may influence bilateral trade, including demographic and macroeconomic indicators as well as dyadic determinants such as common language, common colonizing country, and common currency. The size of the importing and exporting country's relative spending power measured by gross domestic product (GDP) and population have been shown to be predictors of bilateral relationships. Distance between trading partners trade influences transportation costs between partners creating resistance Geographical proximity can be an important factor in negotiating trade agreements that can be a favorable means to secure export markets and

**Table 1. Poultry Product Categories Used in Bilateral Trade Analyses** 

| Product Short<br>Name    | Product Name  | HS<br>Code | HT-SUR<br>Model |
|--------------------------|---|------------|-----------------|
| Whole Chicken:<br>Fresh  | Commodity: 020711, Meat and Edible Offal of Chickens, Not Cut in Pieces, Fresh or Chilled   | 20711      | Fresh           |
| Whole Chicken:<br>Frozen | Commodity: 020712, Meat and Edible Offal of Chickens, Not Cut in Pieces, Frozen   | 20712      | Frozen          |
| Chicken Parts:<br>Fresh  | Commodity: 020713, Chicken Cuts and Edible Offal (Including Livers) Fresh or Chilled  | 20713      | Fresh           |
| Chicken Parts:<br>Frozen | Commodity: 020714, Chicken Cuts and Edible Offal (Including Livers) Frozen  | 20714      | Frozen          |
| Whole Turkey:<br>Frozen  | Commodity: 020725, Turkeys, Not Cut in Pieces, Frozen   | 20725      | Frozen          |
| Whole Turkey:<br>Fresh   | Commodity: 020726, Turkey Cuts and Edible Offal (Including Livers), Fresh or Chilled  | 20726      | Fresh           |
| Turkey Parts:<br>Frozen  | Commodity: 020727, Turkey Cuts and Edible Offal (Including Liver) Frozen  | 20727      | Frozen          |
| Shell Eggs               | Commodity: 0407, Birds' Eggs, In Shell, Fresh, Preserved or Cooked  | 407        | Eggs            |
| Eggs Products            | Commodity: 0408, Birds' Eggs, Not in Shell and Egg Yolks, Fresh, Dried, Cooked by Steam etc., Molded, Frozen or Otherwise Preserved, Sweetened or Not | 408        | Eggs            |
| <b>Cooked Turkey</b>     | Commodity: 160231, Meat or Meat Offal of Turkeys, Prepared or Preserved, N.E.S.O.I.   | 160231     | Prepared        |
| <b>Cooked Chicken</b>    | Commodity: 160232, Prepared or Preserved Chicken Meat, Meat Offal or Blood, N.E.S.O.I.  | 16032      | Prepared        |
| Cooked Other             | Commodity: 160239, Meat or Meat Offal of Chickens, Ducks, Geese and Guineas, Prepared or Preserved, N.E.S.O.I.  | 160239     | Prepared        |

Source: Global Trade Information System – Global Trade Atlas

HS: Harmonized System.

HT-SUR: Hausman-Taylor Seemingly Unrelated Regression

increase trade flows between participating countries (Sunge and Mapfumo 2014). However, an exhaustive set of variables might not be available for every trade relationship, which limits the ability of the model to fully capture multilateral resistance between partners.

In response to these shortcomings of the gravity model of trade, a general form was proposed by Anderson and van Wincoop (2003) to account for multilateral resistance between trading partners. The general form of the gravity model uses partner binary variables to capture the heterogeneity between trading partners without explicitly defining the cultural, political, and economic factors that may influence trade, including binary variables that account for cultural and economic heterogeneity as well as changes in price of the imported good over time (Vollrath and Hallahan 2011). By generalizing the gravity model, the specified nuances from the original model are reduced to country-specific effects which are tractable and provide a robust analysis for works focused on the impacts of exogenous trade shocks. Anderson and van Wincoop use bilateral trade, importer-by-time, and exporter-by-time binary variables to account for time-specific variation in trade by partner and stand in for creation, attraction, and resistance parameters. The general form of the gravity model with time-by-partner variables is shown in Equation 3:

(3) 
$$ln Y_{i,j,t} = K + \beta_1 Pair_{i,j,t} + \beta_2 Pair_{i,t} + \beta_3 Pair_{j,t} + \varepsilon_{i,j,t}$$

where  $Pairs_{i,j} = 1$  if exporter i traded with importer j in time t and 0 otherwise;  $Pairs_{i,t} = 1$  if exporter i traded in time t and 0 otherwise;  $Pairs_{j,t} = 1$  if exporter j traded in time t and 0 otherwise. The importer- and exporter-specific variables incorporate the variation associated with markets that are explicitly modeled in the gravity model.

This work employs the general gravity model to account for individual bilateral partnerships to empirically estimate the impacts of an animal disease event. Simplifying the model to include bilateral pair-specific trade relationships captures nuances of trade, accounting for unique trade relationships and their influence on quantity traded while allowing for focus on the disease event variables. The dependent variable, quantity traded, is linearized after adjusting for zero trade flows to facilitate estimation, as presented in Equation 4:

(4) 
$$\ln q_{i,i,t}^k = \beta_0 + \beta_1 HPAI_{i,t} + \beta_2 NDV_{i,t} + \beta_3 Pairs_{i,j,t} + \gamma Z + \varepsilon_{i,j}$$

where: i= exporter, j= importer, k= product category, t= time, HPAI is a binary variable indicating an HPAI disease event in exporter i for time t, NDV is a binary variable indicating an NDV disease event in exporter i for time t, Pairs is a binary variable for each distinct trading partnership i to j trading in time t, t0 matrix of additional explanatory variables, and t2 matrix of additional explanatory variables, and t3 matrix of additional explanatory variables, and t4 matrix of additional explanatory variables, and t5 matrix of additional explanatory variables, and t6 matrix of additional explanatory variables, and t7 matrix of additional explanatory variables, and t7 matrix of additional explanatory variables, and t8 matrix of additional explanatory variables and t8 matrix of additional explanatory variables.

These data can be estimated as cross-sectional using ordinary least squares (OLS). Although a cross-sectional analysis can provide valuable insights, it does not incorporate information associated with the time aspects of the underlying panel data, thus motivating a panel data approach.

A random effect approach is appropriate if no individual effects are present (Baltagi, Bresson, and Pirotte 2003). If this assumption is rejected, a fixed effect model can be used. However, fixed effect models have limitations in simultaneously providing parameters for time invariant variables and estimations that can be extrapolated to the underlying population. Taking into account both the within and between variation in a panel, a consistent and efficient estimator for a robust, multilevel panel is the Hausman-Taylor (HT) estimator (Hausman and Taylor 1981). The HT estimator assumes the regressors are correlated with the individual effects, so it separates the variables into four categories (Equation 5): 1) time variant exogenous  $(X_1)$ ; 2) time variant endogenous  $(X_2)$ ; 3) time invariant exogenous  $(W_1)$ ; and 4) time invariant endogenous (W2). Equation 4's linearized model variables are separated into respective HT categories (Table 2) and estimated using Equation 5:

(5) 
$$y_{i,t} = \beta_1 X_{1i,t} + \beta_2 X_{2i,t} + \delta_1 W_{1i,t} + \delta_2 W_{2i,t} + \alpha_i + \varepsilon_{i,t}$$

where: i = bilateral trade flows, t = monthly time period,  $\beta$  and  $\delta$  are estimated coefficients for factors that affect trade, y is quantity traded,  $\alpha$  are the individual effects, and  $\varepsilon$  = estimated residuals. Matrix dimension of i is N and tis T such that  $y_{i,t}$  is NTx1. The error term becomes a composite term including both  $\alpha_i$  and  $\varepsilon_{it}$ .

The endogenous variables are assumed to be correlated with the individual effects  $(\alpha_i)$ . The assumption still holds that all variables are uncorrelated with the error term,  $E[\epsilon_{i,t} \mid W_{i,i,t}, X_{i,i,t}] = 0$ , but now the HT estimator expands the model assumptions such that not all variables are uncorrelated with the individual effects, E  $[\alpha_i \mid W_{2i,t}, X_{2i,t}] \neq 0$ .

The HT estimator is a multistep process that approximates the time invariant variables through an instrumental variable approach using the time variant exogenous variables as instruments for the time invariant endogenous variables. This approach makes it possible to generate estimates that can be predictive of the underlying population and include unbiased estimates of relevant time invariant variables, which are limitations of fixed effects models.

Traditionally, when a dataset is multidimensional such as in this study, a researcher must choose which dimension(s) to collapse, or averaging over that dimension, to facilitate estimation, which can reduce the efficiency of the analysis, or choose to estimate M equations (where M is the number of unique identifiers in the data's third dimension). For example, if the third dimension is product type, k (e.g., whole chicken or frozen turkey), and only select products have a response to some external factor such as a disease event, collapsing the data across these commodities might lead to statistically

Table 2. Descriptive Statistics and Hausman-Taylor (HT) Model Descriptions for Variables Used in Bilateral Quantity Trade Analyses

| Name   | Variable Description                                  | Unit   | HT <sup>b</sup> Description   | Mean    | Min  | Max         |  |
|--|---|--------|-------------------------------|---------|------|-------------|--|
| Quantity <sup>a</sup>                          | Quantity of Product Exported                          | Pounds | TV <sup>c</sup> , Exogenous   | 281,484 | 1    | 120,000,000 |  |
| Newcastle Disease<br>Virus (NDV)               | Binary variable indicating if NDV was reported        | 0,1    | TV, Endogenous                | 0.02    | 0    | 1           |  |
| Highly Pathogenic<br>Avian Influenza<br>(HPAI) | Binary variable indicating if HPAI was reported       | 0,1    | TV, Endogenous                | 0.07    | 0    | 1           |  |
| Recession                                      | Binary variable indicating the Great Recession        | 0,1    | TV, Endogenous                | 0.15    | 0    | 1           |  |
| Share  | Annual share of world export market                   | %      | TV, Endogenous                | 0.05    | 0.00 | 0.33        |  |
| Per Capita                                     | Annual global per capita consumption of poultry meat  | %      | TV, Exogenous                 | 12.15   | 10.7 | 13.74       |  |
| OutYear <sub>t</sub>                           | The number of simultaneous disease events in year $t$ | Count  | TV, Exogenous                 | 5.28    | 0    | 15          |  |
| Pairs <sup>e</sup> <sub>i,j,t</sub>            | Indicator for trading partnerships                    | 0,1    | TIV <sup>d</sup> , Endogenous | 0.03    | 0    | 1           |  |
| Asia   | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.10    | 0    | 1           |  |
| Europe   | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.70    | 0    | 1           |  |
| South America                                  | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.03    | 0    | 1           |  |
| North America                                  | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.06    | 0    | 1           |  |
| Africa   | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.06    | 0    | 1           |  |
| Oceania  | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.01    | 0    | 1           |  |
| Middle East                                    | Binary variable for exporting country                 | 0,1    | TIV, Exogenous                | 0.04    | 0    | 1           |  |

Source: Authors Calculations

<sup>&</sup>lt;sup>a</sup>Dependent Variable

<sup>&</sup>lt;sup>b</sup>HT Description = Hausman Taylor variable description

<sup>&</sup>lt;sup>c</sup>TV: Time Variant

<sup>&</sup>lt;sup>d</sup>TIV: Time Invariant

 $e^{i} = \text{exporter}; j = \text{importer}; t = \text{time}$ 

insignificant estimates of disease impacts for aggregated data. However, there may be statistically significant impacts estimated for a specific product had it been modeled individually. While M individual models can be estimated consistently, the limitation is that these models do not account for correlations in the error terms across the models, if present.

A system of Hausman-Taylor estimations (HT-SUR) was first presented by Egger and Pfaffermayr (2004) to address limitations in panel estimators across three-dimensional data. While HT-SUR is applicable across many fields of research, it has been mainly applied in the political economy literature to assess the political factors influencing trade (Angulo, López, and Mur 2011; Serlenga and Shin 2007). Very few studies have employed this methodology in the agricultural trade literature (Slangen, Beugelsdijk, and Hennart 2011).

The HT-SUR creates a system of HT estimations which expand the original estimation to a system of k models instead of individual models. The key relevant aspect of this approach is that the variance of the estimator incorporates not only the combined variance of the within and between estimators but also includes the variance across the individual HT estimators to capture efficiency gains in estimation. Equation 6 presents the expansion of the HT model to *k* models:

(6) 
$$y_{i,t}^{k} = X_{1i,t}'\beta_1 + X_{2i,t}'\beta_2 + W_{1i,t}'\delta_1 + W_{2i,t}'\delta_2 + \alpha_i + \varepsilon_{i,t}$$

where i is the unique identifier, t is time, k is the third dimension (e.g., poultry product categories), and the other variables are defined above.

The HT-SUR uses the same methodological process as the HT estimator, except there is a stacking of equations. This implies that the dimensions of y change from NTx1 to NTKx1, where each NTx1 matrix is stacked by k, or the third dimension (e.g., poultry product categories). The variance is no longer  $\sigma^2$ I for each individual model, but now implies  $\Sigma \otimes I$  where diagonal components are individual model variance covariance matrices and off diagonal components are the covariance between individual models. To empirically estimate the impact on quantity traded as a result of a disease event, a system of models is estimated for poultry product categories and will be compared to individually estimated models as well as alternative estimators.

#### Data

The robust and unique dataset used for this article include HPAI and NDV poultry disease events. These data include 71 disease events affecting 383 distinct bilateral trade relationships for 12 poultry product categories from January 2004 to December 2014. Information concerning the disease events are available on the OIE website, which includes the number of infected flocks, the number of outbreaks during a disease event, and the nature (e.g., zoonotic or only affecting wildlife) of the disease event (OIE 2015). Using these categorizations, individual disease events are recorded in geopolitically defined countries that are non-endemic for HPAI or NDV, where an endemic disease is one that is persistent in a population without external influences.

Bilateral trade data for this article are compiled from the IHS Markit's Global Trade Atlas. Monthly bilateral trade data are used for 24 exporting countries, which attempts to ensure at least 24 months prior to a disease event and 24 months after the OIE declared the country disease free, are included. Bilateral trade is limited to trade relationships that accounted for more than five percent of total exports from each reporting country in 2013, a base year with relatively fewer global outbreaks compared to any other year in the dataset. Limiting trade to more than 5 percent of total exports excludes importing countries that have economically less substantial trading relationships or variable trade quantities for reasons extending beyond animal and food health concerns. These intermittent trading partners that are excluded tended to trade one to two months in any given year, often skipping years. Additionally, this excludes non-recognized trading partners such as "High Seas" and "International Waters."

An incidental benefit of removing the inconsistent and extremely infrequent trading partners is that this allows for better management of zeros in the dataset. Zeros in trade data can be problematic. Alternative estimators have been reviewed to address this issue (Burger, van Oort, and Linders 2009). Balancing data by including zeros can create trade relationships that do not exist, creating a mass of observations at the origin, skewing the results, and creating a substantial mass of very small errors in the disturbance term that violates the normal distribution assumption (Anderson 2010). Although there are very few legitimate zero trade flows (i.e., a partner reduces trade to zero) posted due to reporting lags, transportational lags, or misreporting, for this study, legitimate zero trade flows were recorded as an arbitrarily small number (0.0001) so that these would not be excluded from the log transformed data for estimation and reduce biases created by balancing the trade data or omitting the zero trade flows.

The trade data spans from 2004 to 2015 for 12 poultry product categories, as presented in Table 1, based on the HS six-digit level, which is the lowest HS level consistently reported between all trading partners. The dataset is multidimensional: (1) bilateral trade flows, (2) monthly periods, and (3) product categories. For additional information regarding the dataset used in this article, see Johnson et al. (2015).

<sup>&</sup>lt;sup>1</sup> The countries included are Austria, Belgium, Brazil, Canada, Chile, China, Denmark, France, Germany, Greece, Hungary, Italy, Japan, Mexico, Netherlands, Poland, South Korea, Spain, Sweden, Switzerland, Taiwan, Turkey, the United Kingdom, and the United States.

<sup>&</sup>lt;sup>2</sup> It was possible that a repeat disease event occurred within the 24-month post-disease period that made it impossible to have the 24-month period disease-free buffer around the first event.

Additional information included in the analysis are publicly available data. Summary statistics for the variables used in the analysis are listed in Table 2. The HT variable designation is provided to indicate whether a variable is time variant or time invariant, as well as endogenous or exogenous. Summary statistics are provided for the original data prior to linearization of appropriate variables for Equation 4, a step that occurs prior to estimation. These additional variables are included in the analysis through the Z matrix in Equation 4, which allows for the analysis to extend beyond accounting for individual trading partnerships to provide meaningful insights into capturing factors that influence trade. Share is the exporting country's annual share of the world market for poultry exports and is used to approximate the relative global importance of the exporter on the market. An exporting country's global share can affect how trading partners make trade restriction decisions. Per capita is the annual per capita consumption of poultry meat, which provides a variable to account for the global trend in consumption of poultry products across time.

The dataset includes the Great Recession, a global recession spanning from December 2007 to June 2009, according to the National Bureau of Economic Research (2016). A variable, Recession, is included to account for the changes in trade associated with these economic contractionary periods rather than allow the variations in trade to be associated with preferences for specific poultry products or included in the error term.

The two key disease event variables are NDV and HPAI. NDV is a binary variable that provides an estimate for the marginal effect an NDV disease event has on quantity traded. Similarly, HPAI estimates the marginal trade impacts that occur with an HPAI disease event. Both NDV and HPAI marginal effects provide information for the change in quantity traded and insights into the change in composition of trade between bilateral partners due to a highly pathogenic disease event by product category. The composition of trade is the complete mix of product categories being imported by a trading partner and can change as a result of preferences, risk concerns, or trade response to a disease event. In terms of model specification, disease events have a twofold effect: the exogenous impacts of disease events on quantity traded and the endogenous impacts of country-specific decisions made by animal health authorities which could include regionalization and market switching, both of which influence the quantity traded (Thompson 2018; Webb, Gibson, and Strutt 2018). Because of the relationship between the disease variables and the country's individual effects, both disease variables of interest are modeled as time variant and endogenous.

Out Year, a count of simultaneous disease events for the reporting year, is a global poultry health measure. The number of exporting countries known to be managing a disease event can influence importing partners' trading decisions.

To account for multilateral resistance, individual binary variables are included for each trading partnership, Pairs<sub>i,i,t</sub> accounts for variability around GDP, distance, population, common language, meat consumption preferences, risk perceptions, changes in prices, etc. These variables reduce the need for further multilateral resistance to be modeled.

Finally, there are regional binary variables that account for region-specific exporter characteristics. While trading partners variation is accounted for with the variable  $Pairs_{i,j,b}$  there are regional differences in trade agreements, willingness to accept product from infected exporters, and risk aversion tied to the decision of when to resume trade, all of which are accounted for by the regional variables. The seven regional variables include: Asia, Europe, South America, North America, Africa, Oceania, and the Middle East.

#### **Results and Discussion**

The results are broken out into two components. The first component is the specification of each model and a discussion of each modeling method implemented in this article. The second component is the resulting parameter estimates for the impacts a highly pathogenic disease event has on bilateral trade of disaggregated poultry commodities. The contribution of this article is not only in estimating the impacts of a disease event but also in evaluating modeling estimators.

# **Estimator Specification**

An OLS model with robust standard errors is estimated and presented as *Ordinary Least Squares* model in Table 3. A random effects model uses all information across the multilevel panel, and is also estimated (presented as *Random Effects*). To determine whether true random effects exist or if OLS regression is the consistent and efficient estimator, the random effects model results were tested using a Breusch-Pagan Lagrangian Multiplier (LM) test (Breusch and Pagan 1980). The presence of random effects was statistically different from zero, thereby necessitating the panel approach.

A Hausman specification test was performed to determine whether a random or fixed effects model is more appropriate by testing whether there were individual effects that are correlated with the error term (Hausman 1978). The models fail to meet the asymptotic assumptions of the Hausman test, thus revealing the presence of individual effects consistent with the literature (Baltagi, Bresson, and Pirotte 2003). A fixed effects model is appropriate for the data given these individual effects but limits the analysis to between or within variation estimators. In order to capture both variations, HT and HT-SUR estimators were used.

Using the HT and HT-SUR estimators, there were two approaches modeled. The first approach is to estimate individual HT models, including individual commodity models (presented as *Individual Hausman-Taylor*) as well as a combined HT model (presented as *Combined Hausman-Taylor*) that uses disease-commodity interaction variables to determine the commodity-specific impacts of a disease outbreak in a single model. The second approach is to

Table 3. Comparison of Disease Coefficient Results for Estimated Quantity Traded of Poultry Products, 2004 to 2015

|                         | OLS              |                      | Random Effects   |                      | Combined HT <sup>1</sup> |                    | Individual HT <sup>2</sup> |                     | Reduced<br>Individual HT <sup>3</sup> |                   | HT-SUR <sup>4</sup> |                   |
|-------------------------|------------------|----------------------|------------------|----------------------|--------------------------|--------------------|----------------------------|---------------------|---------------------------------------|-------------------|---------------------|-------------------|
|                         | NDV              | HPAI                 | NDV              | HPAI                 | NDV                      | HPAI               | NDV                        | HPAI                | NDV                                   | HPAI              | NDV                 | HPAI              |
| Whole Fresh<br>Chicken  | 0.15*<br>(0.08)  | -0.19***<br>(0.07)   | 0.15*<br>(0.08)  | -0.19***<br>(0.07)   | 0.13<br>(0.10)           | -0.24***<br>(0.08) | 0.15*<br>(0.08)            | -0.19***<br>(0.07)  | 0.10<br>(0.06)                        | -0.24**<br>(0.10) | 0.17<br>(0.32)      | -0.27*<br>(0.16)  |
| Whole Frozen<br>Chicken | 0.10<br>(0.07)   | -0.02 (0.06)         | 0.10<br>(0.07)   | -0.02 (0.06)         | 0.23***<br>(0.07)        | 0.09<br>(0.07)     | 0.10<br>(0.07)             | -0.02 (0.06)        | 0.38<br>(0.46)                        | 0.13<br>(0.30)    | 0.38<br>(0.46)      | 0.12<br>(0.32)    |
| Fresh Chicken<br>Parts  | 0.07<br>(0.07)   | -0.18***<br>(0.05)   | 0.07<br>(0.07)   | -0.18***<br>(0.05)   | 0.08<br>(0.09)           | -0.21*** (0.07)    | 0.07<br>(0.07)             | -0.18***<br>(0.05)  | 0.13***<br>(0.05)                     | 0.08<br>(0.06)    | 0.25<br>(0.18)      | 0.23**<br>(0.09)  |
| Frozen Chicken<br>Parts | -0.10*<br>(0.06) | $-0.15*** \\ (0.04)$ | -0.10*<br>(0.06) | $-0.15*** \\ (0.04)$ | -0.11 (0.07)             | -0.17*** (0.05)    | $-0.10* \\ (0.06)$         | $-0.15*** \ (0.04)$ | 0.19<br>(0.18)                        | 0.06<br>(0.08)    | 0.19<br>(0.13)      | 0.02<br>(0.09)    |
| Whole Frozen<br>Turkey  | -0.13 (0.17)     | 0.45***<br>(0.15)    | -0.13 (0.17)     | 0.45***<br>(0.15)    | 0.04<br>(0.14)           | 0.64***<br>(0.13)  | -0.13 (0.17)               | 0.45***<br>(0.15)   | -0.65 (1.31)                          | 2.84**<br>(1.13)  | -0.65 (1.49)        | 2.83***<br>(1.04) |
| Whole Fresh<br>Turkey   | -0.08 (0.08)     | -0.16***<br>(0.05)   | -0.08 (0.08)     | -0.16***<br>(0.05)   | -0.05 (0.11)             | -0.12*<br>(0.07)   | -0.08 (0.08)               | -0.16***<br>(0.05)  | 0.19<br>(0.12)                        | -0.07 (0.06)      | 0.19<br>(0.20)      | -0.07 (0.10)      |
| Frozen Turkey<br>Parts  | 0.06<br>(0.06)   | 0.13**<br>(0.05)     | 0.06<br>(0.06)   | 0.13**<br>(0.05)     | 0.10<br>(0.08)           | 0.18***<br>(0.06)  | 0.06<br>(0.06)             | 0.13**<br>(0.05)    | -0.17 (0.44)                          | -0.10 (0.26)      | -0.17 (0.27)        | -0.12 (0.19)      |
| Shell Eggs              | 0.02<br>(0.15)   | 0.23**<br>(0.10)     | 0.02<br>(0.15)   | 0.23**<br>(0.10)     | 0.09<br>(0.08)           | 0.31***<br>(0.05)  | 0.02<br>(0.15)             | 0.23**<br>(0.10)    | -0.12 (0.20)                          | 0.36**<br>(0.16)  | -0.12 (0.22)        | 0.37***<br>(0.14) |
| Egg Products            | 0.11*            | 0.04                 | 0.11*            | 0.04                 | 0.08                     | -0.05              | 0.11*                      | 0.04                | -0.04                                 | 0.17***           | -0.04               | 0.17***           |
|                         | (0.07)           | (0.06)               | (0.07)           | (0.06)               | (80.0)                   | (0.07)             | (0.07)                     | (0.06)              | (0.05)                                | (0.04)            | (0.07)              | (0.04)            |
| Cooked Turkey           | 0.12             | 0.16***              | 0.12             | 0.16***              | 0.19**                   | 0.23***            | 0.12                       | 0.16***             | -0.24***                              | 0.02              | -0.24**             | 0.02              |
|                         | (80.0)           | (0.06)               | (80.0)           | (0.06)               | (0.09)                   | (0.07)             | (80.0)                     | (0.06)              | (0.09)                                | (0.10)            | (0.10)              | (0.09)            |

**Table 3. Continued** 

|                | OLS          |        | Random Effects |        | Combined HT <sup>1</sup> |        | Individual HT <sup>2</sup> |        | Reduced<br>Individual HT <sup>3</sup> |        | HT-SUR <sup>4</sup> |         |
|----------------|--------------|--------|----------------|--------|--------------------------|--------|----------------------------|--------|---------------------------------------|--------|---------------------|---------|
|                | NDV          | HPAI   | NDV            | HPAI   | NDV                      | HPAI   | NDV                        | HPAI   | NDV                                   | HPAI   | NDV                 | HPAI    |
| Cooked Chicken | 0.23***      | -0.01  | 0.23***        | -0.01  | 0.09                     | -0.09* | 0.23***                    | -0.01  | 0.03                                  | -0.11  | 0.03                | -0.11** |
|                | (80.0)       | (0.05) | (80.0)         | (0.05) | (0.09)                   | (0.05) | (80.0)                     | (0.05) | (0.04)                                | (0.08) | (0.06)              | (0.06)  |
| Cooked Other   | 0.00         | 0.10   | 0.00           | 0.10   | -0.16                    | -0.01  | 0.00                       | 0.10   | -0.05                                 | 0.10   | -0.05               | 0.10    |
|                | (0.11)       | (0.07) | (0.11)         | (0.07) | (0.11)                   | (0.06) | (0.11)                     | (0.07) | (0.08)                                | (0.07) | (0.09)              | (80.0)  |
| Observations   | 1,872-11,063 |        | 1,872-11,063   |        | 82,380                   |        | 1,872-11,063               |        | 478-3,981                             |        | 478-3,981           |         |

<sup>&</sup>lt;sup>1</sup>Combined Hausman-Taylor model, including fixed effect variables for specified commodities.

<sup>&</sup>lt;sup>2</sup>Individual Hausman-Taylor models estimated for each of the commodities. (12 models)

<sup>&</sup>lt;sup>3</sup>Inidvidual Hausman-Taylor models using reduced data for consistent comparison to HT-SUR models. (12 models)

<sup>&</sup>lt;sup>4</sup>Hausman-Taylor seemingly unrelated regression for the fresh, frozen, eggs, and prepared models. (4 systems of 12 total models) Note: Standard errors in parentheses. \*\*\*, \*\*\*, and \* indicate p < 0.01, p < 0.05, and p < 0.1, respectively.

capture potential efficiency gains in estimation using the HT-SUR applied over groupings of product categories (see Table 1) and are presented as Hausman-Taylor Seemingly Unrelated Regression model (Table 3). Each system of equations was tested for independent equations using the Breusch-Pagan LM test. For every system presented—Fresh, Frozen, Eggs, and Prepared—the null hypothesis of independent equations was rejected, allowing for modeling efficiency with the HT-SUR approach.

There are limitations of the second approach that lie with an unbalanced panel, which limits the data that can be used. Given the HT-SUR requires a balanced panel to estimate, observations, or partnerships that do not trade every product category in a system, were excluded. This translates into a change from 52 trading partners on average for all 12 categories for the individual models to 13 trading partners for the HT-SUR. Without creating trading partnerships that do not exist for specific products and creating a substantial mass of very small errors in the disturbance term that violates the normal distribution assumption (Anderson 2010), the bilateral trading pairs that were used in the HT-SUR estimation are limited. In order for a comparison of potential efficiency gains, individual models were re-estimated only including the observations that were used in the HT-SUR estimation and presented as *Reduced Individual Hausman-Taylor* model Consistently, the results show little to no efficiency gains (in terms of reduced standard errors) in using the HT-SUR model over comparable individual modeling, with the trade-off being usable data. Due to limitations in selection criteria for HT modeling, there are no advanced methods for selecting the optimal model. The best alternative is to use the adjusted R<sup>2</sup> value as the indicator for superior model selection, given the same independent variables are included in all models. The HT model adjusted R2 values ranged from 0.616-0.922, whereas the HT-SUR models ranged from 0.616-0.948, indicating slight value in estimating the system over the individual models.

# Estimated Disease Impact Results and Discussion

Estimates for the impact an HPAI or NDV disease event has on quantity traded are presented in Table 3 for models discussed above: Ordinary Least Squares, Random Effects, Individual Hausman-Taylor Models (HT), Combined Hausman-Taylor Model, Reduced Hausman-Taylor Models, and the Hausman-Taylor Seemingly Unrelated Regression (HT-SUR). Full results are available upon request to the authors.

Using the Individual Hausman-Taylor Model estimations, NDV events tend to significantly impact select chicken products. Of the five chicken products, NDV events significantly impact whole fresh, frozen parts, and cooked chicken products. The response across these products vastly differs from a 23 percent increase in cooked chicken quantity traded during an outbreak to a decrease in quantity traded by 10 percent for frozen chicken parts. Additionally, egg products show a significant increase (11 percent) in exports during an NDV event. These results indicate a change in composition of trade. The composition, or mix of products, being traded is also an important aspect of bilateral trade. While total quantity across all poultry products may decrease during a disease event, these results decompose trade into product-specific changes. Changes in product trade during an outbreak can be attributed to many factors, including preferences of trading partners for further processed products or increases in advantageous trade as a result of more affordable products that some importing partners are willing to accept. Advantageous product category pricing could explain the estimated increase in whole fresh chicken trade, as it becomes relatively less expensive. Neighboring partners, where further processing occurs after shipment, could also increase import demand for fresh products. For example, the United States ships the majority (77 percent during the 2013 base year) of whole fresh chicken exports to Mexico, providing for reduced transportation costs and flexibility in composition of products exported.

The NDV results are similar in nature when comparing the HT individual models to the combined model. While the coefficients change in significance from one model to the next, when determining whether the coefficients are statistically different across the models, we fail to reject the hypothesis that they were the same. While trading partners can use these estimates to understand the effect an NDV event has on quantity traded, NDV events comprise a relatively small portion of the panel data. Although NDV events account for 45 percent of all disease events in the data, they affect less than 2 percent of the bilateral trade observations. This small portion of affected trade was driven by the duration of an NDV event from the first reported outbreak until the last reported outbreak. NDV events affect less than 3 percent of the reported trade lasting more than a year, whereas this is closer to 18 percent of trade for HPAI events. Importing counties can have a trade response to any animal health or food safety event, but an explanation for why NDV does not significantly contribute to changes in trade might be tied to the relative short disease durations and possible zoonotic capability.

In comparison to NDV events, HPAI events were estimated to be a significant factor of quantity traded for most of the poultry product categories in the HT individual models. For all individual models other than whole frozen chicken, cooked chicken, and cooked other, the *HPAI* variable is significant at the 95 percent significance level. This implies that in terms of trade quantity impacts, HPAI is a disease of greater importance across all poultry product categories than NDV.

Results show statistically significant decreases in quantity traded due to an HPAI event for chicken categories. For example, an HPAI event leads to a 19 percent decrease in whole fresh chicken exports and an 18 percent decrease in fresh chicken parts. This is consistent with expectations around chicken exports reductions due to shortage of exporter supply and importer responses. Cooked chicken was not significantly impacted due to an HPAI event. This could imply that while there may be reductions in exporter

supply of cooked chicken, there might be an increase in demand for these further processed products to mitigate some risk of disease spread.

Contrarily, turkey product category exports were estimated to have varying trade responses which can represent changes in composition of turkey trade. Whole fresh turkey exports are estimated to decrease by 16 percent during an outbreak, while whole frozen turkey, frozen turkey parts, and cooked turkey are expected to increase by 45 percent, 13 percent, and 16 percent, respectively. Countries that import poultry meat typically import frozen products (61 percent of meat products exported in 2013 were frozen products), possibly due to their hardiness to withstand transportation. During an outbreak, there may be a change in importers' share of exports to those who prefer frozen turkey over fresh turkey meat. Similar results were found in the combined model. The values vary in magnitude, but just as in chicken poultry product categories, the two model coefficients were not statistically different.

Shell eggs have a significant increase in quantity traded on average, 23 percent, during an HPAI outbreak, while egg products were not significantly impacted. An a priori expectation would anticipate a decrease in the trade of these sensitive products, as shown during the 2014-2015 HPAI event in U.S. egg layers. However, the counterintuitive results lie with the estimation and the bilateral trading partners' relationships in the data. That is, the estimated results show the average response between bilateral pairs, but this does not imply that every partnership increases trade for shell eggs during an HPAI event. Additionally, shell egg trade is generally driven between contiguous partners such as Belgium and Netherlands, Canada and the United States, or Iraq and Turkey. Of the top ten exporters for shell eggs, seven exporters are part of the European Union and account for 52 percent of shell egg trade. During an outbreak, where the importing partner might also be infected or processing facilities are across national borders, such as within the European Union, the increases in trade could be due to reduction in importer domestic supply.

Until this point, the discussion has focused on the HT models but has not accounted for factors that affect multiple categories simultaneously or correlation across error terms. To address these correlations, the HT-SUR models were estimated, capturing the relationships across the models. However, due to estimation limitations, observations were dropped for the HT-SUR models. The models are tested for independent equations using the Breusch-Pagan LM statistic, and results reject the hypothesis independence. Thus, the HT-SUR results can be compared to the Reduced Hausman-Taylor Models (Table 3). Coefficients were consistent across both reduced observation estimators, and there were negligible differences in standard errors. While there might be theoretical gains in choosing to estimate a system of equations rather than individual models, the trade-off is a reduction in usable bilateral partners.

To understand the impacts of that trade-off, the HT-SUR results can be compared to the HT models. Directionally, the coefficients have similar results for all categories except cooked turkey between the HT and HT-SUR methods. The magnitude of the impact of a highly pathogenic disease event tend to be greater in the reduced models than for the HT models, where the complete data were used. For example, the HT-SUR estimates a 283 percent increase in whole frozen turkey trade during an HPAI event compared to a 45 percent increase in the HT models. This large discrepancy is due to the bilateral partners used in the HT-SUR, where the bilateral partners tended to be European partners which might have a disproportionate trade response not applicable to all exporters. Cooked turkey trade quantity changes as a result of a disease impact was the only category in which the sign changes between the HT models and HT-SUR models, driven by the remaining pairs sample specific responses. With the unbalanced nature of the available data, analyzing product categories instead of aggregated commodities, the HT models provide a better representation of the effects across exporters than the HT-SUR estimator.

### Conclusion

Many factors affect global poultry trade, including proximity, product and country reputation, demand preferences, and available trade supplies. Highly pathogenic poultry disease events can cause disruptions in trade flows through changes in supplies and through importer trade restrictions leading to changes in quantity traded, composition of products traded, and sources of imports. This study estimates the impacts HPAI and NDV events have on quantity traded by comparing a series of estimators. The results provide a deeper understanding of disease events' trade impacts. These impacts can be used to anticipate potential changes in poultry product category quantity traded during periods of disease planning and response and, consequently, enable an exporter to adapt more quickly to changes in importers' trade composition based on preferences and the price of exports.

The individual product category model results suggest that HPAI events tend to have a greater impact across all poultry product categories when compared to NDV events and indicate a greater vulnerability of poultry meat and poultry product export markets during HPAI disease events. While NDV does have an impact on trade, particularly for cooked chicken, HPAI has a significant impact on bilateral trade across most poultry product categories. This could be due to the short duration of NDV events, the highly prolific nature of HPAI, or the more numerous strains of HPAI with zoonotic potential. However, this information does reveal differing trade responses and risk perceptions associated with specific poultry diseases. The results reinforce the importance of disease mitigation strategies domestically for highly pathogenic poultry diseases and the importance of biosecurity for reducing potential disease pathways.

Analyzing trade flows by product category allows for product categoryspecific changes to be estimated and provides valuable insights for production decisions in the face of a disease event. For aggregated analyses,

the actual change in composition is not parsed out, and estimations can over or underestimate the impact of the factors affecting trade with no understanding of the nuances in changes to trade composition. By understanding the trade implications of disease event, pre-event contingency planning might both alleviate some of the economic strain that the events pose and aid in market recovery. Future research could focus on one commodity and further explore the temporal and dynamic nature of disease impacts.

Using the Hausman-Taylor Seemingly Unrelated Regression (HT-SUR) estimator, this article bridges the gap from the political economy literature to agricultural trade in showing a consistent and efficient estimator for multidimensional data. The use of the HT-SUR allows researchers to maintain data dimensionality, not typical of panel data analyses in the agricultural economics literature, where some form of aggregation across one of the dimensions can smooth out potential effects of explanatory variables. By using the HT-SUR, aggregation is not necessary, providing a framework for a three-dimensional analysis. While there are limitations with the HT-SUR, this does not discount the method's potential use across disciplines and data. Using this methodology, future work could include other agricultural sectors to estimate the effects of major trade-distorting events to improve the available information to exporting and importing countries. Future research with balanced panels could benefit from using this methodology to estimate three-dimensional datasets where the limitations would not be an issue with a balanced panel.

#### **Financial Statement**

This material is based on work supported by the U.S. Department of Homeland Security under Cooperative Agreement Number DHS 2010-ST-061-AG0002 and the U.S. Department of Agriculture under Cooperative Agreement Number 14-9200-0374. The views and conclusions in this document are those of the authors and should not be interpreted as necessarily representing the official polices, either expressed or implied, of the U.S. Department of Homeland Security, the Institute for Infectious Animal Diseases, or the U.S. Department of Agriculture.

# **Conflicts of Interest**

None.

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